LISTING OF THE CLAIMS

1. (Withdrawn) A method of amplifying genomic fragments, comprising the steps:

digesting genomic DNA into genomic fragments, wherein said digesting results in genomic fragment overhangs;

contacting said genomic fragments with one or more adapters, wherein said adapters are complementary to at least two of said overhangs;

ligating said adapters to said genomic fragment overhangs to form closed adapter-genomic fragment circles;

separating said adapter-genomic fragment circles from linear fragments; and

amplifying said adapter-genomic fragment circles.

2. (Withdrawn) A method of amplifying genomic fragments, comprising the steps:

digesting genomic DNA into genomic fragments, wherein said digesting results in genomic fragment overhangs;

contacting said genomic fragments with one or more adapters, wherein said adapters are complementary to at least two of said overhangs;

ligating said adapters to said genomic fragment overhangs to form closed adapter-genomic fragment circles;

modifying said circles by cutting with one or more restriction enzymes binding to one or more adapter sites; and

amplifying said adapter-genomic fragment circles.

3. (Withdrawn) The method of claim 1 or 2, wherein said digestion is performed by a Type IIS enzyme.

4. (Withdrawn) The method of claim 2 wherein said restriction enzyme is a Type IIS enzyme.

5. (Withdrawn) The method of claim 3 or 4, wherein said Type IIS enzyme is selected from the consisting of Bbv I, SfaN 1, Fok I, BsmF I, and BsmA I.

6. (Withdrawn) The method of claim 3, wherein said enzyme has a specific recognition site and a separate digestion site.

7. (Withdrawn) The method of claim 5, wherein said enzyme has a four-, five-, or six-base recognition sequence.

8. (Withdrawn) The method of claim 1 or 2, wherein said overhangs are two, three or four bases long.

9. (Withdrawn) The method of claim 1 or 2, wherein said amplification is selected from the group consisting of rolling circle PCR and inverse PCR.

10. (Withdrawn) The method of claim 1 or 2, wherein said adapters comprise one or two pairs of Type IIS restriction enzyme recognition sites, each pair positioned at one adapter end for cutting into the genomic and adapter DNA thereby forming matching overhang sequences.

11. (Withdrawn) The method of claim 1 or 2, wherein uracil is incorporated into the adapter sequence.

12. (Withdrawn) The method of claim 12, wherein the adapter is treated with uracil-DNA glycosylase prior to amplification.

13. (Withdrawn) The method of claim 1, wherein said separating is performed by digesting said linear fragments with an enzyme.

14. (Withdrawn) The method of claim 13, wherein said enzyme is an exonuclease.

15. (Withdrawn) The method of claim 1, wherein said separating is performed by biotinylated blocking adaptors and streptavin-coated beads combined with magnetic attraction or centrifugation.

16. (Withdrawn) The method of claim 15, wherein said biotinylated blocking adapters comprise a first and a second end, said first end having an overhang complimentary to said overhangs of said universal adapters, and said second end covalently bound to at least one biotin molecule.

17. (Withdrawn) The method of claims 1 or 2, wherein at least one blocking adapter is included in the ligating step.

18. (Currently amended) Two sets of universal building blocks comprising:

a first set of single-stranded oligonucleotides having a first end and a second end, said first end having a sticky-end overhang and said second end having sequence of 8-20 bases; and a second set of single-stranded oligonucleotides having a first end and a second

end, said first end having a sticky-end overhang and said second end having a sequence of 8-20 bases, wherein said first ends of said first and second sets are different, and said second end of said first set are complementary to said second end of said second set, generating all possible combinations of adapter sequences, and wherein each second end of each oligonucleotide in said first set has the same sequence and each second end of each oligonucleotide in said second set has the same sequence, and wherein each of said first set and said second set comprise a minimum of two oligonucleotides each which form at least four adaptor sequences.

19. (Original) The sets of universal building blocks of claim 18, wherein said first and second set are comprised of up to 64 different first end 3-base overhangs.

20. (Original) The sets of universal building blocks of claim 18, wherein said first and second set are comprised of up to 256 different first end 4-base overhangs.

21. (Original) The sets of universal building blocks of claim 18, wherein said first and second set are comprised of up to 1024 different first end 5-base overhangs.

22. (New) The set of universal building blocks of claim 18, wherein adaptor sequences generated from hybridization of oligonucleotides in said first set to oligonucleotides in said second set are in an amount equal to the number of oligonucleotides in said first set multiplied by the number of oligonucleotides in said second set.